## WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid molecule that comprises a polynucleotide sequence that encodes a polypeptide selected from the group consisting of:

a) a polypeptide having lipid A biosynthesis acyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 70% identical to an amino acid sequence encoded by nucleotides 350-1234 (ORF 2a) of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

b) a polypeptide having glycosyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 70% identical to an amino acid sequence encoded by nucleotides 1234-2487 (ORF 3a) of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

c) a polypeptide having glycosyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 50 % identical to an amino acid sequence encoded by nucleotides 2786-3952 (ORF 4a) of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1 over a region at least about 100 amino acids in length;

d) a polypeptide having β1,4-GalNAc transferase activity, wherein the GalNAc transferase polypeptide comprises an amino acid sequence that is at least about 77% identical to an amino acid sequence as set forth in SEQ ID NO:17 over a region at least about 50 amino acids in length;

e) a polypeptide having β1,3-galactosyltransferase activity, wherein the galactosyltransferase polypeptide comprises an amino acid sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:27 or SEQ ID NO:29 over a region at least about 50 amino acids in length;

f) a polypeptide having α2,3 sialyltransferase activity, wherein the sialyltransferase polypeptide comprises an amino acid sequence that is at least about 66% identical over a region at least about 60 amino acids in length to an amino acid sequence as set forth in one or more of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7 or SEQ ID NO:10;

g) a polypeptide having sialic acid synthase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 70% identical to an amino acid sequence encoded by nucleotides 6924-7961 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

h) a polypeptide having sialic acid biosynthesis activity, wherein the polypeptide comprises an amino acid sequence that is at least about 70% identical to an amino acid sequence encoded by nucleotides 8021-9076 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

i) a polypeptide having CMP-sialic acid synthetase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 65% identical to an amino acid sequence encoded by nucleotides 9076-9738 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

j) a polypeptide having acetyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 65% identical to an amino acid sequence encoded by nucleotides 9729-10559 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1; and

k) a polypeptide having glycosyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 65% identical to an amino acid sequence encoded by a reverse complement of nucleotides 10557-11366 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1.

2. The isolated or recombinant nucleic acid molecule of claim 1, wherein the nucleic acid comprises a polynucleotide sequence that encodes one or more polypeptides selected from the group consisting of:

a) a sialyltransferase polypeptide that has both an α2,3 sialyltransferase activity and an α2,8 sialyltransferase activity, wherein the sialyltransferase polypeptide comprises an amino acid sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:3 over a region at least about 50 amino acids in length;

b) a GalNAc transferase polypeptide that has a β1,4-GalNAc transferase activity, wherein the GalNAc transferase polypeptide comprises an amino acid

sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:17 over a region at least about 50 amino acids in length; and

c) a galactosyltransferase polypeptide that has β1,3-galactosyltransferase activity, wherein the galactosyltransferase polypeptide comprises an amino acid sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:27 over a region at least about 50 amino acids in length.

3. The nucleic acid molecule of claim 1, wherein the sequence comparisons are performed using a BLASTP Version 2.0 algorithm with a wordlength (W) of 3, G=11, E=1, and a BLOSUM62 substitution matrix.

4. The nucleic acid molecule of claim 1, wherein the region extends the full length of the amino acid sequence of the polypeptide.

5. The nucleic acid molecule of claim 1, wherein:

a) the sialyltransferase polypeptide comprises an amino acid sequence as set forth in SEQ ID NO:3, SEQ ID NO:5 SEQ ID NO:7 or SEQ ID NO:10;

b) the GalNAc transferase polypeptide comprises an amino acid sequence as set forth in SEQ ID NO:17; and

c) the galactosyltransferase polypeptide comprises an amino acid sequence as set forth in SEQ ID NO:27 or SEQ ID NO:29.

6. The nucleic acid molecule of claim 5, wherein:

a) the polynucleotide sequence that encodes the sialyltransferase polypeptide is at least about 75% identical to a nucleic acid sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6 over a region at least about 50 nucleotides in length;

b) the polynucleotide sequence that encodes the β1,4-GalNAc transferase polypeptide is at least about 75% identical to a nucleic acid sequence as set forth in SEQ ID NO:16 or over a region at least about 50 nucleotides in length; and

c) the polynucleotide sequence that encodes the β1,3-galactosyltransferase polypeptide is at least about 75% identical to a nucleic acid sequence

as set forth in SEQ ID NO:26 or SEQ ID NO:28 over a region at least about 50 nucleotides in length.

7. The nucleic acid molecule of claim 6, wherein the sequence comparisons are performed using a BLASTN Version 2.0 algorithm with a wordlength (W) of 11, G=5, E=2, q= -2, and r = 1.

8. The nucleic acid molecule of claim 6, wherein:

a) the polynucleotide sequence that encodes the sialyltransferase polypeptide has an nucleic acid sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:6;

b) the polynucleotide sequence that encodes the GalNAc transferase polypeptide has a nucleic acid sequence as set forth in SEQ ID NO:16; and

c) the polynucleotide sequence that encodes the galactosyltransferase polypeptide has a nucleic acid sequence as set forth in SEQ ID NO:26 or SEQ ID NO:28.

9. The nucleic acid molecule of claim 5, wherein the sialyltransferase is a bifunctional sialyltransferase that has both an $\alpha$2,3-sialyltransferase activity and an $\alpha$2,8-sialyltransferase activity and the polynucleotide sequence that encodes the sialyltransferase polypeptide is at least about 75% identical to a nucleic acid sequence as set forth in SEQ ID NO:2, SEQ ID NO:4.

10. An expression cassette that comprises a nucleic acid molecule of claim 1.

11. An expression vector that comprises the expression cassette of claim 10.

12. A host cell that comprises the expression vector of claim 11.

13. An isolated or recombinantly produced polypeptide selected from the group consisting of:

a) a polypeptide having lipid A biosynthesis acyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 70% identical to an amino acid sequence encoded by nucleotides 350-1234 (ORF 2a) of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

b) a polypeptide having glycosyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 70% identical to an amino acid sequence encoded by nucleotides 1234-2487 (ORF 3a) of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

c) a polypeptide having glycosyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 50 % identical to an amino acid sequence encoded by nucleotides 2786-3952 (ORF 4a) of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1 over a region at least about 100 amino acids in length;

d) a polypeptide having β1,4-GalNAc transferase activity, wherein the GalNAc transferase polypeptide comprises an amino acid sequence that is at least about 77% identical to an amino acid sequence as set forth in SEQ ID NO:17 over a region at least about 50 amino acids in length;

e) a polypeptide having β1,3-galactosyltransferase activity, wherein the galactosyltransferase polypeptide comprises an amino acid sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:27 or SEQ ID NO:29 over a region at least about 50 amino acids in length;

f) a polypeptide having α2,3 sialyltransferase activity, wherein the sialyltransferase polypeptide comprises an amino acid sequence that is at least about 66% identical to an amino acid sequence as set forth in SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7 or SEQ ID NO:10 over a region at least about 60 amino acids in length;

g) a polypeptide having sialic acid synthase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 70% identical to an amino acid sequence encoded by nucleotides 6924-7961 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

h) a polypeptide having sialic acid biosynthesis activity, wherein the polypeptide comprises an amino acid sequence that is at least about 70% identical to an amino acid sequence encoded by nucleotides 8021-9076 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

i) a polypeptide having CMP-sialic acid synthetase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 65% identical to an amino acid sequence encoded by nucleotides 9076-9738 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1;

j) a polypeptide having acetyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 65% identical to an amino acid sequence encoded by nucleotides 9729-10559 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1; and

k) a polypeptide having glycosyltransferase activity, wherein the polypeptide comprises an amino acid sequence that is at least about 65% identical to an amino acid sequence encoded by a reverse complement of nucleotides 10557-11366 of the *LOS* biosynthesis locus of *C. jejuni* strain OH4384 as shown in SEQ ID NO:1.

14. The isolated or recombinantly produced polypeptide of claim 13, wherein the polypeptide is recombinantly produced and at least partially purified.

15. The isolated or recombinantly produced polypeptide of claim 13, wherein the polypeptide is expressed by a heterologous host cell.

16. The isolated or recombinantly produced polypeptide of claim 15, wherein the host cell is *E. coli*.

17. The isolated or recombinantly produced polypeptide of claim 13, wherein the polypeptide is a *C. jejuni* serotype O:2 polypeptide.

18. The isolated or recombinantly produced polypeptide of claim 13, wherein the polypeptide is a sialyltransferase polypeptide according to g) and the polypeptide is selected from the group consisting of:

a polypeptide has both an α2,3 sialyltransferase activity and an α2,8 sialyltransferase activity and comprises an amino acid sequence that is at least 75% identical to an amino acid sequence of a *cstII* sialyltransferase encoded by ORF 7a of the *LOS* biosynthesis locus from *C. jejuni* strain OH4384 as set forth in SEQ ID NO:3;

a polypeptide that has an α2,3 sialyltransferase activity and comprises an amino acid sequence that is at least 75% identical to an amino acid sequence of a *cst*II sialyltransferase from *C. jejuni* serotype O:10 as set forth in SEQ ID NO:5;

a polypeptide that that has an α2,3 sialyltransferase activity and comprises an amino acid sequence that is at least 75% identical to an amino acid sequence of a *cst*II sialyltransferase from *C. jejuni* serotype O:41 as set forth in SEQ ID NO:7; and

a polypeptide that that has an α2,3 sialyltransferase activity and comprises an amino acid sequence that is at least 75% identical to an amino acid sequence of a *cst*II sialyltransferase of *C. jejuni* serotype O:2 as set forth in SEQ ID NO:10.

19. The isolated or recombinantly produced sialyltransferase polypeptide of claim 18, wherein the sialyltransferase polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, and SEQ ID NO:10.

20. The polypeptide of claim 13, wherein:

a) the sialyltransferase polypeptide of f) has an amino acid sequence as set forth in SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7 or SEQ ID NO:10;

b) the 1,4-GalNAc transferase polypeptide of d) has an amino acid sequence as set forth in SEQ ID NO:17; and

c) the β1,3-galactosyltransferase polypeptide of e) has an amino acid sequence as set forth in SEQ ID NO:27 or SEQ ID NO:29.

21. A reaction mixture for synthesis of a sialylated oligosaccharide, the reaction mixture comprising a sialyltransferase polypeptide which has both an α2,3 sialyltransferase activity and an α2,8 sialyltransferase activity, a galactosylated acceptor moiety, and a sialyl-nucleotide sugar;

wherein the sialyltransferase transfers a first sialic acid residue from the sialyl-nucleotide sugar to the galactosylated acceptor moiety in an α2,3 linkage, and further transfers a second sialic acid residue to the first sialic acid residue in an α2,8 linkage.

22. The reaction mixture of claim 21, wherein the sialyl-nucleotide sugar is CMP-sialic acid.

23. The reaction mixture of claim 21, wherein the sialyltransferase polypeptide has an amino acid sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:3 over a region at least about 50 amino acids in length.

24. The reaction mixture of claim 23, wherein the sialyltransferase polypeptide has an amino acid sequence as set forth in SEQ ID NO:3.

25. The reaction mixture of claim 21, wherein the galactosylated acceptor comprises a compound having the formula Galβ1,4-R or Galβ1,3-R, wherein R is selected from the group consisting of H, a saccharide, oligosaccharide, or an aglycone group having at least one carbohydrate atom.

26. The reaction mixture of claim 21, wherein the galactosylated acceptor is attached to a protein, lipid, or proteoglycan.

27. The reaction mixture of claim 21, wherein the sialylated oligosaccharide is a ganglioside, a ganglioside mimic, or a carbohydrate portion of a ganglioside.

28. The reaction mixture of claim 21, wherein the sialylated oligosaccharide is a lysoganglioside, a lysoganglioside mimic, or a carbohydrate portion of a lysoganglioside.

29. The reaction mixture of claim 27, wherein the galactosylated acceptor moiety comprises a compound having a formula selected from the group consisting of Gal4Glc-$R^1$ and Gal3GalNAc-$R^2$; wherein $R^1$ is selected from the group consisting of ceramide or other glycolipid, and $R^2$ is selected from the group consisting of Gal4GlcCer, (Neu5Ac3)Gal4GlcCer, and (Neu5Ac8Neu5c3)Gal4GlcCer.

30. The reaction mixture of claim 29, wherein the galactosylated acceptor is selected from the group consisting of Gal4GlcCer, Gal3GalNAc4(Neu5Ac3)Gal4GlcCer, and Gal3GalNAc4(Neu5Ac8Neu5c3)Gal4GlcCer.

31. The reaction mixture of claim 21, wherein the galactosylated acceptor is formed by contacting an acceptor saccharide with UDP-Gal and a galactosyltransferase polypeptide, wherein the galactosyltransferase polypeptide transfers the Gal residue from the UDP-Gal to the acceptor.

32. The reaction mixture of claim 31, wherein the galactosyltransferase polypeptide has β1,3-galactosyltransferase activity and has an amino acid sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:27 or SEQ ID NO:29 over a region at least about 50 amino acids in length.

33. The reaction mixture of claim 32, wherein the galactosyltransferase has an amino acid sequence as set forth in SEQ ID NO:27 or SEQ ID NO:29.

34. The reaction mixture of claim 31, wherein the acceptor saccharide comprises a terminal GalNAc residue.

35. The reaction mixture of claim 34, wherein the acceptor saccharide for the galactosyltransferase is formed by contacting an acceptor for a GalNAc transferase with UDP-GalNAc and a GalNAc transferase polypeptide, wherein the GalNAc transferase polypeptide transfers the GalNAc residue from the UDP-GalNAc to the acceptor for the GalNAc transferase.

36. The reaction mixture of claim 35, wherein the GalNAc transferase polypeptide has a β1,4-GalNAc transferase activity and has an amino acid sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:17 over a region at least about 50 amino acids in length.

37. The reaction mixture of claim 29, wherein the GalNAc transferase polypeptide has an amino acid sequence as set forth in SEQ ID NO:17.

38. A method for synthesizing a sialylated oligosaccharide, the method comprising incubating a reaction mixture that comprises a sialyltransferase polypeptide which has both an α2,3 sialyltransferase activity and an α2,8 sialyltransferase activity, a galactosylated acceptor moiety, and a sialyl-nucleotide sugar, under suitable conditions wherein the sialyltransferase polypeptide transfers a first sialic acid residue from the sialyl-nucleotide sugar to the galactosylated acceptor moiety in an α2,3 linkage, and further transfers a second sialic acid residue to the first sialic acid residue in an α2,8 linkage.

39. The method of claim 38, wherein the sialylated oligosaccharide is a ganglioside.

40. The method of claim 38, wherein the sialyltransferase polypeptide has an amino acid sequence that is at least about 75% identical to an amino acid sequence as set forth in SEQ ID NO:3 over a region at least about 50 amino acids in length.

41. The method of claim 40, wherein the sialyltransferase polypeptide has an amino acid sequence as set forth in SEQ ID NO:3.

42. The method of claim 38, wherein the sialylated oligosaccharide is a ganglioside a lysoganglioside, a ganglioside mimic, or a lysoganglioside mimic.